W217

QTLs from Genome to Field Using Markers and Genetic Maps for Peanut Improvement

Date: Saturday, January 12, 2013
Time: 3:10 PM
Room: Pacific Salon 1

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Peanut (*Arachis hypogaea*) is widely grown in the semi-arid tropics regions of Asia, Africa and Latin America where several stress factors together adversely affect productivity. Collaborative efforts led development of large scale genomic resources setting platform for genomics-assisted breeding (GAB). GAB promises to foster genetic enhancement leading to increased productivity, drought tolerance, disease resistance and improved oil quality in groundnut which are otherwise difficult through conventional breeding alone. In this context, after screening a total of 4,245 SSR markers on parental genotypes of five mapping populations, individual genetic maps with 83-191 marker loci were constructed. Using marker segregation data from 11 populations, a reference consensus genetic map was developed with 897 marker loci which was then further enriched upto 3,693 marker loci by adding mapping information from five new genetic maps. Detailed QTL analyses provided 153 QTLs for drought tolerance related traits, 43 QTLs for foliar diseases (late leaf spot and leaf rust) and 49 QTLs for oil quality. A major QTL contributing upto 82.96% phenotypic variation for rust resistance has been introgressed into three elite peanut varieties namely ICGV 91114, JL 24 and TAG 24 using marker-assisted backcrossing. Disease screening of 200 introgression lines in advanced generation (117 BC_2F_5 and 83 BC_3F_5) have recorded a rust score of 2 (scale 1 to 9). The promising lines with desirable yield and higher resistance to leaf rust could be released an improved varieties. Integration of such genomics approaches in breeding programme will enhance crop productivity of groundnut.